

Figure 1a**Variable Heavy Chain DNA****3077_VH1B (SEQ ID NO: 1):**

(1) CAGGTGCAAT TGGTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
 (51) CGTAAAGTG AGCTGAAAG CCTCCGGATA TACCTTACT TCTTATTCTA
 (101) TTAATTGGGT CCGCCAAGCC CCTGGCAGG GTCTCGAGTG GATGGGCTAT
 (151) ATCGATCCGA ATCGTGGAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
 (201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACGTGA
 (251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
 (301) ATTTATTTA TTCATGGTAT GCTTGATTT TGGGGCAAG GCACCCCTGGT
 (351) GACGGTTAGC TCA

3079_VH3 (SEQ ID NO: 2):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CCTCCGGATT TACCTTTCT AATTATGGTA
 (101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCCGTTCTG ATGGTAGCTG GACCTATTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAAA CACCGTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTCGTTAT
 (301) TGGTCTAAGT CTCATGCTTC TGTTACTGAT TATTGGGCC AAGGCACCCCT
 (351) GGTGACGGTT AGCTCA

3080_VH3 (SEQ ID NO: 3):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CCTCCGGATT TACCTTTCT TCTTATGGTA
 (101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCTATTCTG ATGGTAGCAA TACCTTTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAAA CACCGTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTAATATG
 (301) TATCGTTGGC CTTTCATTA TTTTTTGAT TATTGGGCC AAGGCACCCCT
 (351) GGTGACGGTT AGCTCA

3100_VH3 (SEQ ID NO: 4):

(1) CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
 (51) CCTGCGTCTG AGCTGCGCG CCTCCGGATT TACCTTTCT TCTAATGGTA
 (101) TGTCTTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
 (151) ATCTCTTATC TTTCTAGCTC TACCTATTAT GCGGATAGCG TGAAAGGCCG
 (201) TTTTACCAATT TCACGTGATA ATTGAAAAA CACCGTGTAT CTGCAAATGA
 (251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTTTAT
 (301) GGTTATTTA ATTATGCTGA TGTTGGGCC CAAGGCACCC TGGTGACGGT
 (351) TAGCTCA

3077_1_VH1B (SEQ ID NO: 31):

(1) CAGGTGCAAT TAGTCCAAAG TGGTGCAGGAA GTGAAAAAAC CGGGCGCGAG
 (51) CGTAAAGTG AGCTGAAAG CCTCCGGATA TACCTTACT TCTTATTCTA

(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTA TTCATGGTAT GCTTGATTT TGGGGCCAAG GCACCCCTGGT
(351) GACGGTTAGC TCA

Figure 1b**Variable Heavy Chain Peptide**
(CDR Regions in Bold)**3077_VH1B (SEQ ID NO: 5):**

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYSINWVRQA PGQGLEWMGY
(51) IDPNRGNTNY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCAREY
(101) IYFIHGMLDF WGQGTLVTVS S

3079_VH3 (SEQ ID NO: 6):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS NYGMHWVRQA PGKGLEWVSN
(51) IRSDDGSWTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARRY
(101) WSKSHASVTD YWGQGTLVTV SS

3080_VH3 (SEQ ID NO: 7):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVSN
(51) IYSDGSNTFY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARNM
(101) YRWPFFHYFFD YWGQGTLVTV SS

3100_VH 3 (SEQ ID NO: 8):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS SNGMSWVRQA PGKGLEWVSN
(51) ISYLSSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARFY
(101) GYFNYADVWG QGTLVTVSS

Figure 2a

Variable Light Chain DNA

3077_Vk kappa 2 (SEQ ID NO: 9):

(1) GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
 (51) GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTT TTTATTGATG
 (101) GCAATAATTA TCTGAATTGG TACCTTCAAA AACCAAGTCA AAGCCCGCAG
 (151) CTATTAATTTC ATCTTGGTTC TAATCGTGCC AGTGGGGTCC CGGATCGTTT
 (201) TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
 (251) AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGTATTG TTCTAAGTCT
 (301) GCTACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG

3079_Vk kappa 1 (SEQ ID NO: 10):

(1) GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
 (51) TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGATATTCT GCTTTCTGA
 (101) ATTGGTACCA GCAGAAACCA GGTAAGCAC CGAAACTATT AATTATAAG
 (151) GTTTCTAATT TGCAAAGCGG GGTCGGTCC CGTTTAGCG GCTCTGGATC
 (201) CGGCACTGAT TTTACCCCTGA CCATTAGCAG CCTGCAACCT GAAGACTTG
 (251) CGACTTATTAA TTGCCAGCAG GCTTATTCTG GTTCTATTAC CTTTGGCCAG
 (301) GGTACGAAAG TTGAAATTAA ACGTACG

3080_Vl lambda 3 (SEQ ID NO: 11):

(1) GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
 (51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTAATAAG TATGTTTCTT
 (101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTGTTGTGAT TTATGGTGAT
 (151) AATAATCGTC CCTCAGGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
 (201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
 (251) ATTATTATTG CTCTTCTTAT GATTCTTCTT ATTTTGTTGTT TGGCGCGGC
 (301) ACGAAGTTAA CCGTTCTTGG CCAG

3100_Vl lambda 3 (SEQ ID NO: 12):

(1) GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
 (51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTCATTAT TATGCTTCTT
 (101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTTGTGAT TTATCGTGAT
 (151) AATGATCGTC CCTCAGGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
 (201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
 (251) ATTATTATTG CCAGTCTTAT GATTATCTTC ATGATTGTT GTTGGCGGC
 (301) GGCACGAAGT TAACCGTTCT TGGCCAG

Figure 2b**Variable Light Chain Peptide**
(CDR Regions in **Bold**)**3077_Vk kappa 2 (SEQ ID NO: 13):**

(1) DIVMTQSPLS LPVTPGEPAS ISCRESSQSLL **FIDGNNYLNW** YLQKPGQSPQ
(51) LLIYLGSNRA **SGVPDRFSGS** GSGTDFTLKI SRVEAEDVGV YYCQQYSSKS
(101) ATFGQGTKVE IKRT

3079_Vk kappa 1 (SEQ ID NO: 14):

(1) DIQMTQSPSS LSASVGDRVT ITCRASQDIS AFLNWYQQKPG GKAPKLLIYK
(51) VSNLQSGVPS RFSGSGSGTD FTLLTISSLQP EDFATYYCQQ **AYSGSITFGQ**
(101) GTKVEIKRT

3080_Vl lambda 3 (SEQ ID NO: 15):

(1) DIELTQPPSV SVAPGQTARI SCSSGDNIGNK YVSWYQQKPG QAPVVVIYGD
(51) NNRPSGIPER FSGSNSGNTA TLTISGTQAE DEADYYCSSY DSSYFVFGGG
(101) TKLTVLGQ

3100_Vl lambda 3 (SEQ ID NO: 16):

(1) DIELTQPPSV SVAPGQTARI SCSSGDNIGHY YASWYQQKPG QAPVLVIYRD
(51) NDRPSGIPER FSGSNSGNTA TLTISGTQAE DEADYYCQSY DYLHDFVFGGG
(101) GTKLTVLGQ

Figure 3

Variable Heavy Chain Consensus Sequences

(CDR Regions in Bold)

VH1B Consensus (SEQ ID NO: 17):

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYVMHWVRQA PGQGLEWMGW
(51) INPNSGGTNY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCARWG
(101) **GDGFYAMDY**W GQGTLTVSS

VH3 Consensus (SEQ ID NO: 18):

(1) QVOLVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA
(51) **ISGSGG**STYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARWG
(101) **GDGFYAMDY**W GQGTLTVVS S

Figure 4**Variable Light Chain Consensus Sequences**(CDR Regions in **Bold**)**VL_λ3 Consensus (SEQ ID NO: 19):**

(1) **SYELTQPPSV** SVAPGQTARI **SCSGDALGDK** YASWYQQKPG QAPVLVIYDD
(51) **SDRPMSGIPER** FSGSNNSGNTA TLTISGTQAE DEADYYCQQH YTTPPVFGGG
(101) TKLTVLG

VL_k1 Consensus (SEQ ID NO: 20):

(1) **DIQMTQSPSS** LSASVGDRVT **ITCRASQGIS** SYLAWYQQKP GKAPKLLIYA
(51) **ASSLQSGVPS** RFSGSGSGTD FTLTISSLQP EDFATYYCQQ **HYTTPPTFGQ**
(101) GTKVEIKR

VL_k2 Consensus (SEQ ID NO: 21):

(1) **DIVMTQSPLS** LPVTPGEPAS **ISCRSSQSLL** HSNGNYLDW YLQKPGQSPQ
(51) **LLIYLGSNRA** SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQHYTTP
(101) PTFGQGTKVE IKR

Figure 5**Peptide Sequence of CD38**

(SEQ ID NO: 22):

1 mancefspvs gdkpccrlsr raqlclgvsi lvlilvvla vvvprwrqqw sgpgttkrfp
61 etvlarcvky teihpemrvhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn
121 killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181 snnpvsfvfk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea
241 wvihggreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei

Figure 6**Nucleotide Sequence of Chimeric OKT10****Heavy Chain (SEQ ID NO: 23):**

caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc
 gattttagta gatcctggat gaattgggtc cggcaggctc cagaaaaagg gctagaatgg
 attggagaaa ttaatccaga tagcagtacg ataaaactata cgacatctct aaaggataaa
 ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaattgac caaagtgaga
 tctgaggaca cagcccttta ttactgtgca agatatggta actggttcc ttattggggc
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 gtc当地ggct tctatccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag
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 aagctcaccg tggacaagag caggtggcag cagggaaacg tcttctcatg ctccgtatg
 catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Light Chain (SEQ ID NO: 24):

gatatccctga tgacccagtc tcaaaaaatc atgcccacat cagtggaga cagggtcagc
 gtcacctgca aggccagtca aaatgtggat actaatgttag cctggatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcatcctacc gatacagtgg agtccctgat
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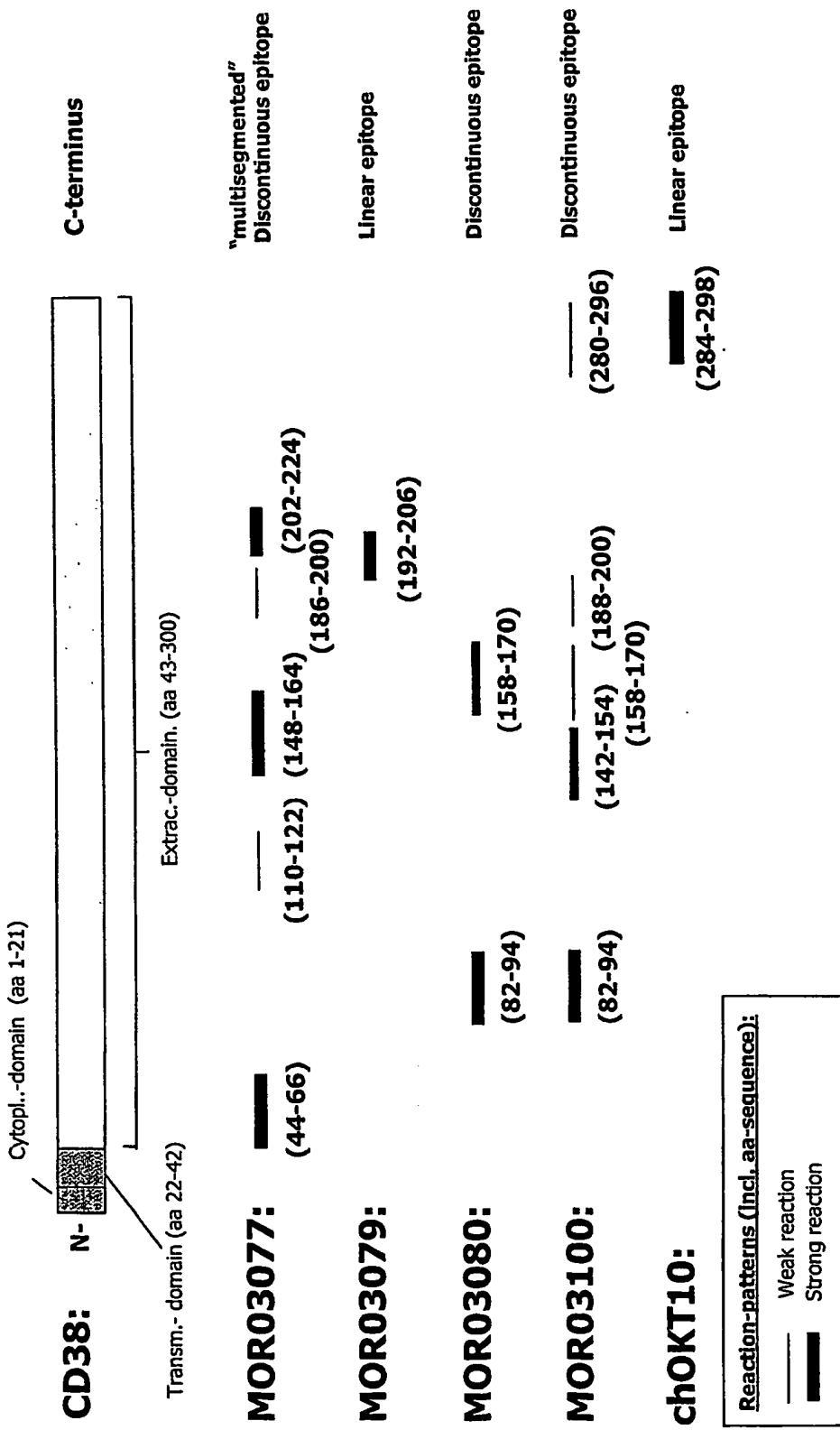
Fig.7: Schematic Overview of Epitopes

Figure 8: DNA sequence of pMOPRH®_h_IgG1_1

StyI

601 TCGCTATTAC CATGGTGTATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

AatII

651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
ATCGCCAAAC TGAGTCCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTCCA AAATGTCGTA
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGAG
TGTTGAGGCG GGGTAACCTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC

801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

pMOPRH®_Ig FOR 100.0%

851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGT CGACCGATCG

M K H L W F F L L L V A A P R

901 GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCCAG
CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

StyI

EcoRI

BlpI

951 . W V L S Q V E F C R R L A Q
ATGGGTCTTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
TACCCAGGAC AGGGTCACC TTAAGACGTC CGCCAATCGA GTCGGAGGTG

StyI

BbsI

1001 . K G P S V F P L A P S S K S T S G
CAAGGGTCCA TCGGTCTTCC CCGTGGCACC CTCCCTCCAAG AGCACCTCTG
GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTC TCGTGGAGAC

1051 . G T A A L G C L V K D Y F P E P
GGGGCACAGC GGCCCTGGC TGCCTGGTCA AGGACTACTT CCCCCAACCG
CCCCGTGTG CGGGGACCCG ACGGACCAAGT TCCTGATGAA GGGGCTTGGC

V T V S W N S G A L T S G V H T F

1101 GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA

P A V L Q S S G L Y S L S S V V T

1151 CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
GGGCGACAG GATGTCAGGA GTCCCTGAGAT GAGGGAGTCG TCGCACCCT

V P S S S L G T Q T Y I C N V N

1201 CCGTGCCTC CAGCAGCTTG GGCAACCCAGA CCTACATCTG CAACGTGAAT
GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACCTA

StyI

H K P S N T K V D K K V E P K S C

1251 CACAAGCCCC GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
GTGTTGGGT CGTTGTGGTT CCACCTGTTT TTTCAACTCG GGTTTAGAAC

D K T H T C P P C P A P E L L G G

1301 TGACAAAACT CACACATGCC CACCGTGCCT AGCACCTGAA CTCTGGGGG
ACTGTTTGAGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

BbsI

1351 GACCGTCAGT CTTCCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
CTGGCAGTCA GAAGGAGAAC GGGGGTTTTG GGTTCCGTGT GGAGTACTAG

StyI

BbsI

S R T P E V T C V V V D V S H E D

1401 TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT

BbsI

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P E V K F N W Y V D G V E V H N A

1451 CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

K T K P R E E Q Y N S T Y R V V

1501 CCAAGACAAA GCCCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
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S V L T V L H Q D W L N G K E Y K

1551 AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
TCGCAGGAGT GGCAGGACGT GGTCTGACC GACTTACCGT TCCTCATGTT

C K V S N K A L P A P I E K T I S

1601 GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
CACGTTCCAG AGGTTTTC GGGAGGGTCG GGGTAGCTC TTTGGTAGA

BsrGI

1651 K A K G Q P R E P Q V Y T L P P
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 GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT

 S R D E L T K N Q V S L T C L V K

1701 TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
 AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAAGTT

 G F Y P S D I A V E W E S N G Q P

1751 AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
 TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCCTCTCG TTACCCGTG

1801 E N N Y K T T P P V L D S D G S
 CGGAGAACAA CTACAAGACC ACGGCTCCCG TGCTGGACTC CGACGGCTCC
 GCCTTTGTT GATGTTCTGG TGCGGAGGGC ACGACCTGAG GCTGCCGAGG

 F F L Y S K L T V D K S R W Q Q G

1851 TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
 AAGAAGGAGA TGTCGTTCGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

BbsI

NsiI

 N V F S C S V M H E A L H N H Y T

1901 GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
 CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

SapI

PmeI

 Q K S L S L S P G K *

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 GCGTCTTCTC GGAGAGGGAC AGAGGCCAT TTACTCCCGG GCAAATTG

2001 CGCTGATCAG CCTCGACTGT GCCTCTAGT TGCCAGCCAT CTGTGTGTTG
 GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

pMORPH_Ig_REV 100.0%

2051 CCCCTCCCCC GTGCCTTCCT TGACCCCTGGGA AGGTGCCACT CCCACTGTCC
 GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG

Figure 9: DNA Sequence of Ig kappa light chain expression vector

pMORPH®_h_Igk_1

StyI

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601 TCGCTATTAC CATGGTGATG CGGTTTGGC AGTACATCAA TGGGCGTGG
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651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCCA TTGACGTCAA
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      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT
      -----
751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGGAG
      TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC
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801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

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pMORPH®_Ig_FOR 100%

NheI

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851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
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      StyI
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      BsiWI
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+1 V T E Q D S K D S T Y S L S S T L
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+1 T L S K A D Y E K H K V Y A C E V
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+1 T H Q G L S S P V T K S F N R G
1251 CACCCATCAG GGCGTGGACT CGCCCCGTCAC AAAGAGCTTC AACAGGGGAG
      GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCCTC

+1 E C *
1301 AGTGTAGGG GCCCGTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCCTCT
      TCACAATCCC CGGGCAAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA

PmeI
1351 AGTTGCCAGC CATCTGTTGT TTGCCCTCTCC CCCGTGCCCTT CCTTGACCCCT
      TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAACGGGA

```

Figure 10: DNA Sequence of HuCAL® Ig lambda light chain vector

pMORPH®_h_Igλ_1

StyI

601 TCGCTATTAC CATGGTGATG CGGTTTGGC AGTACATCAA TGGGCGTGGAA
AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCCA TTGACGTCAA
ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGGAG
TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCCTC

801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTGGGT GACGAATGAC

pM_Ig_FOR 100.0% NheI

851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGT CGACCGATCG

+1 M A W A L L L L T L L T Q G T
StyI

901 GCCACCATGG CCTGGGCTCT GCTGCTCCTC ACCCTCCTCA CTCAGGGCAC
CGGTGGTACC GGACCCGAGA CGACGGAGGAGT GAGTCCCGTG

+2 T V L G Q

+1 G S W A D I V M H E V
BamHI EcoRV HpaI StyI

951 AGGATCCTGG GCTGATATCG TGATGCACGA AGTTAACCGT CCTAGGTCAG
TCCTAGGACC CGACTATAGC ACTACGTGCT TCAATTGGCA GGATCCAGTC

+2 P K A A P S V T L F P P S S E E L
StyI

1001 CCCAAGGCTG CCCCCCTCGGT CACTCTGTT CCGCCCTCCT CTGAGGAGCT
GGGTTCCGAC GGGGGAGCCA GTGAGACAAG GGCGGGAGGA GACTCCTCGA

+2 Q A N K A T L V C L I S D F Y P

1051 TCAAGCCAAC AAGGCCACAC TGGTGTGTCT CATAAGTGAC TTCTACCCGG
AGTCGGTTG TTCCGGTGTG ACCACACAGA GTATTCACTG AAGATGGGCC

+2 G A V T V A W K G D S S P V K A G
 1101 GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
 CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

+2 V E T T T P S K Q S N N K Y A A S
 1151 GTGGAGACCA CCACACCCCTC CAAACAAAGC ACAACAAAGT ACGCGGCCAG
 CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

+2 S Y L S L T P E Q W K S H R S Y
 1201 CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAAGTCCCAC AGAACGCTACA
 GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAAGGGTG TCTTCGATGT

+2 S C Q V T H E G S T V E K T V A P
 BbsI

1251 GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCT
 CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

+2 T E C S *

PmeI

1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
 TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
 pM_Ig_REV 100%

1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
 CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
 pM_Ig_REV 100.0%

Fig. 11: Proliferation Assay

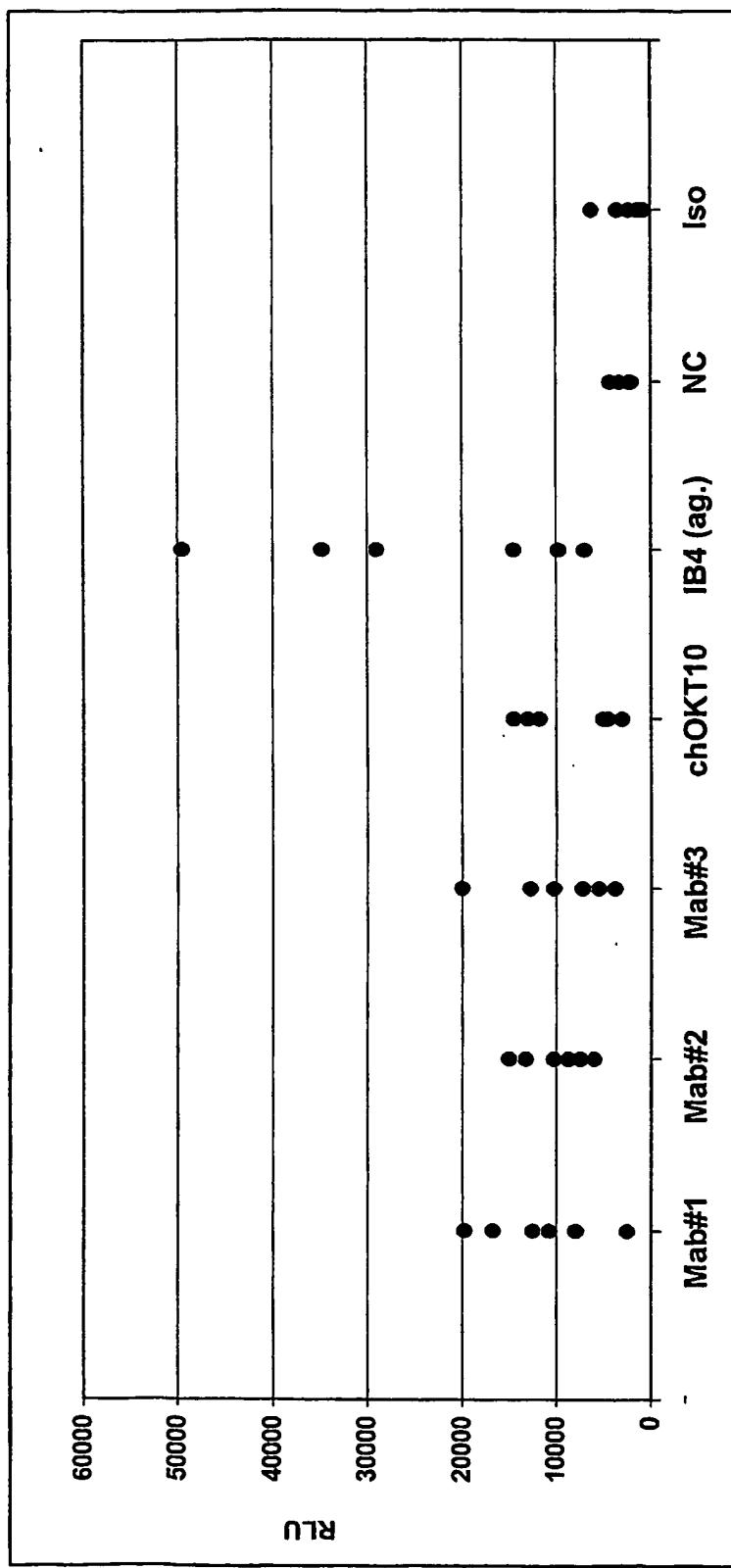


Fig. 12: IL-6 Release Assay

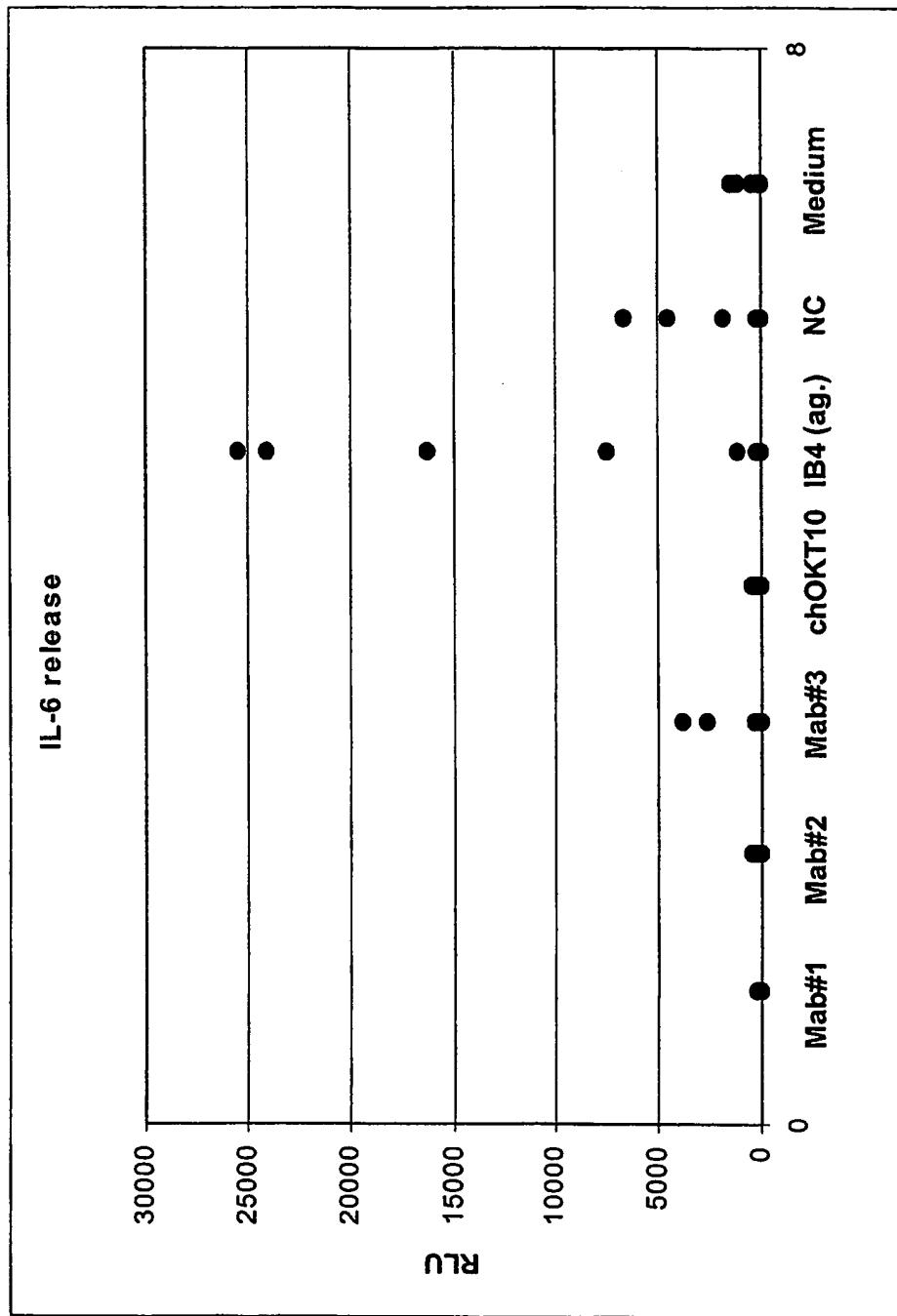


Fig. 13: Cytotoxicity towards CD34+/CD38+ progenitor cells

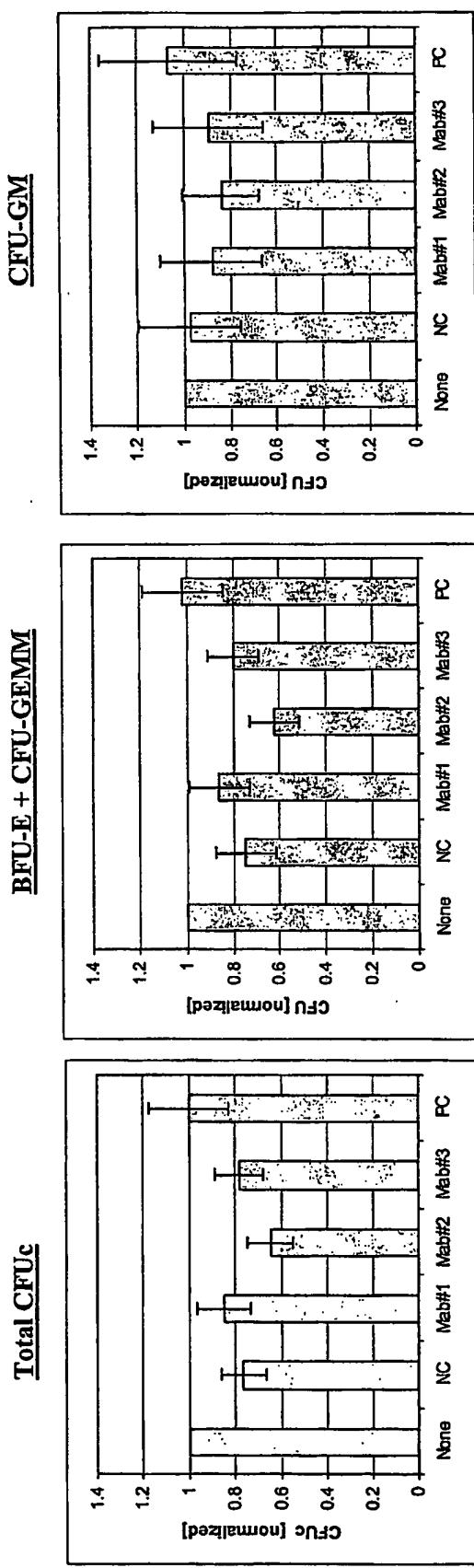


Fig. 14: ADCC with different cell-lines

Cell line	Culture Collection	Origin	Expression [MF1]	Max. specific killing [%] in ADCC ^{a,c}		
				Mab#1	Mab#2	Mab#3
RPMI 8226	ATCC CCL-155	MM	405.71	56	58	54
KMS-12-BM	DSMZ ACC551	MM	142.29	26	32	30
NCI-H929	ECACC95050415	MM	45.01	68	73	38
OPM-2	DSMZ ACC50	MM	37.99	6	13	3
U-266	ECACC85051003	MM	26.14	17	14	12
KMS-11	Nambu <i>et al.</i> , 1989 ^b	MM	26.81 ^c	22	30	26
JVM-13	DSMZACC19	CLL	463.93	11	20	12
JVM-2	DSMZACC12	CLL	140.84	22	28	10
CCRF-CEM	ECACC85112105	ALL	301.46	24	29	20
Jurkat	DSMZ ACC282	ALL	202.99	7	8	13
AML-193	DSMZ ACC549	AML	62.69 ^c	33	26	39
OCI-AML5	DSMZ ACC247	AML	207.55 ^d	20	21	16
NB-4	DSMZ ACC207	AML	164.7 ^d	36	38	32
THP-1	DSMZ ACC16	AML	34.41	64	59	38
HL-60 ^d	DSMZ ACC3	AML	18.43 ^a	29	35	29
Raji	Burkitt's Lymph.	Burkitt's lymph.	n.d.	53	62	48
						n.d.

Fig. 15: ADCC with MM-samples

Antibodies	Mab#1	Mab#2	Mab#3	PC
Parameters:				
MM samples: EC50 [nM] ^a :	0.116-0.202	0.006-0.185	0.027-0.249	0.282-0.356
MM samples: Max spec. killing [%]	13.1 - 61.6	16.2 - 57.9	13.6 - 36.0	15.5 - 49.5

Fig. 16: Treatment of human myeloma xenograft with MOR03080

